



Revised Sequence Listing filed 2006-07-26  
SEQUENCE LISTING

<110> KATO, Seishi  
NAGATA, Naoki  
FUJIMURA, Naoko  
KOBAYASHI, Midori  
ITO, Koichi  
ISHIZUKA, Yoshiko

<120> A Method For Producing An Antibody By Gene Immunization

<130> 2002\_0400A

<140> 10/088,859

<141> 2002-05-29

<150> PCT/JP01/06371

<151> 2001-07-24

<150> PCT2000-222743

<151> 2000-07-24

<150> JP2000-254407

<151> 2000-08-24

<160> 18

<170> PatentIn version 3.3

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aatcaaaacg ctgattaaaa gaagcacggt atg atg acc aaa cat aaa aag tgt 174  
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Phe Ile Ile Val Gly Val Leu Ile Thr Thr Asn Ile Ile Thr Leu Ile  
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gtt aaa cta act cga gat tct cag agt tta tgc ccc tat gat tgg att 270  
Val Lys Leu Thr Arg Asp Ser Gln Ser Leu Cys Pro Tyr Asp Trp Ile  
25 30 35 40

ggg ttc caa aac aaa tgc tat tat ttc tct aaa gaa gaa gga gat tgg 318  
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45 50 55

aat tca agt aaa tac aac tgt tcc act caa cat gcc gac cta act ata 366  
Asn Ser Ser Lys Tyr Asn Cys Ser Thr Gln His Ala Asp Leu Thr Ile  
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75 80 85	
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Ser Asp His Trp Ile Gly Leu Lys Met Ala Lys Asn Arg Thr Gly Gln	
90 95 100	
tgg gta gat gga gct aca ttt acc aaa tcg ttt ggc atg aga ggg agt	510
Trp Val Asp Gly Ala Thr Phe Thr Lys Ser Phe Gly Met Arg Gly Ser	
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Glu Gly Cys Ala Tyr Leu Ser Asp Asp Gly Ala Ala Thr Ala Arg Cys	
125 130 135	
tac acc gaa aga aaa tgg att tgc agg aaa aga ata cac taa	600
Tyr Thr Glu Arg Lys Trp Ile Cys Arg Lys Arg Ile His	
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35 40 45
Phe Ser Lys Glu Glu Gly Asp Trp Asn Ser Ser Lys Tyr Asn Cys Ser
50 55 60
Thr Gln His Ala Asp Leu Thr Ile Ile Asp Asn Ile Glu Glu Met Asn
65 70 75 80
Phe Leu Arg Arg Tyr Lys Cys Ser Ser Asp His Trp Ile Gly Leu Lys
85 90 95
Met Ala Lys Asn Arg Thr Gly Gln Trp Val Asp Gly Ala Thr Phe Thr
100 105 110
Lys Ser Phe Gly Met Arg Gly Ser Glu Gly Cys Ala Tyr Leu Ser Asp
115 120 125

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Ala Val Glu Ala Thr Gly Glu Lys Val Leu Arg Tyr Glu Thr Phe Ile  
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Ser Asp Val Leu Gln Arg Asp Leu Arg Lys Val Leu Asp His Arg Asp  
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Lys Val Tyr Glu Gln Leu Ala Lys Tyr Leu Gln Leu Arg Asn Val Ile  
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Glu Arg Leu Gln Glu Ala Lys His Ser Glu Leu Tyr Met Gln Val Asp  
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Ile Tyr Val Ala Leu Gly Tyr Gly Phe Phe Leu Glu Leu Thr Leu Ala  
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Glu Ala Leu Lys Phe Ile Asp Arg Lys Ser Ser Leu Leu Thr Glu Leu  
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Ser Asn Ser Leu Thr Lys Asp Ser Met Asn Ile Lys Ala His Ile His  
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Phe Phe Leu Glu Leu Thr Leu Ala Glu Ala Leu Lys Phe Ile Asp Arg  
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gag atc tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ttg Glu Ile Tyr Gln Glu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu 110 115 120	387
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Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala	
1 5 10 15	
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Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro	
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Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala	
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Trp Pro Thr Pro Pro Thr Arg Pro Ala Pro Ala Pro Cys His Ala Asn	
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Thr Ser Met Val Thr His Pro Asp Phe Ala Thr Gln Pro Gln His Val	
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Gln Asn Phe Leu Leu Tyr Arg His Cys Arg His Phe Pro Leu Leu Gln	
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Gly	Val	Arg	Ala	Pro	Ser	Gln	His	Leu	Ser	Ser	Phe	Asp	Pro	Cys	Phe	
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tac	cga	gac	ctg	ctg	ctg	gtg	cac	cgc	ttc	cta	cct	tat	gag	atg	ctg	1173
Tyr	Arg	Asp	Leu	Leu	Leu	Val	His	Arg	Phe	Leu	Pro	Tyr	Glu	Met	Leu	



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355 360 365

aca cag atc tac tga gtcagcatca ggggtccccag cctctgggct cctgtttcca 1276  
Thr Gln Ile Tyr  
370

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ctt ctg ggg gcc ctg ctg gga acc gcc tgg gct cgg agg agc cag gat 219  
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90					95				100						105		
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Val	Arg	Val	Val	Gly	Arg	Asn	Gly	Glu	Ser	Ser	Glu	Leu	Asp	Leu	Gln		
				110				115						120			
ggc	atc	cga	atc	gac	tca	gat	att	agc	ggc	acc	ctc	aag	ttt	gcg	tgt		555
Gly	Ile	Arg	Ile	Asp	Ser	Asp	Ile	Ser	Gly	Thr	Leu	Lys	Phe	Ala	Cys		
			125					130					135				
gag	agc	att	gtg	gag	gaa	tac	gag	gat	gaa	ctc	att	gaa	ttc	ttt	tcc		603
Glu	Ser	Ile	Val	Glu	Glu	Tyr	Glu	Asp	Glu	Leu	Ile	Glu	Phe	Phe	Ser		
		140					145					150					
cga	gag	gct	gac	aat	gtt	aaa	gac	aaa	ctt	tgc	agt	aag	cga	aca	gat		651
Arg	Glu	Ala	Asp	Asn	Val	Lys	Asp	Lys	Leu	Cys	Ser	Lys	Arg	Thr	Asp		
	155					160					165						
ctt	tgt	gac	cat	gcc	ctg	cac	ata	tcg	cat	gat	gag	cta	tga				693
Leu	Cys	Asp	His	Ala	Leu	His	Ile	Ser	His	Asp	Glu	Leu					
170					175					180							
accactggag	cagccacac	tggttgatg	gatcacc	cccc	aggagg	gggaa	aatggtggca										753
atgcctttta	tatattatgt	ttttactgaa	attaactgaa	aaaatatgaa	accaaagta												813
c																	814

<210> 12  
 <211> 695  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (73)..(564)

<400> 12  
 aagatttcag ctgcgggacg gtcaggggag acctccaggc gcaggggaagg acggccaggg 60

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tgacacggaa gc atg cga cgg ctg ctg atc cct ctg gcc ctg tgg ctg ggc 111  
Met Arg Arg Leu Leu Ile Pro Leu Ala Leu Trp Leu Gly  
1 5 10

gcg gtg ggc gtg ggc gtc gcc gag ctc acg gaa gcc cag cgc cgg ggc 159  
Ala Val Gly Val Gly Val Ala Glu Leu Thr Glu Ala Gln Arg Arg Gly  
15 20 25

ctg cag gtg gcc ctg gag gaa ttt cac aag cac ccg ccc gtg cag tgg 207  
Leu Gln Val Ala Leu Glu Glu Phe His Lys His Pro Pro Val Gln Trp  
30 35 40 45

gcc ttc cag gag acc agt gtg gag agc gcc gtg gac acg ccc ttc cca 255  
Ala Phe Gln Glu Thr Ser Val Glu Ser Ala Val Asp Thr Pro Phe Pro  
50 55 60

gct gga ata ttt gtg agg ctg gaa ttt aag ctg cag cag aca agc tgc 303  
Ala Gly Ile Phe Val Arg Leu Glu Phe Lys Leu Gln Gln Thr Ser Cys  
65 70 75

cgg aag agg gac tgg aag aaa ccc gag tgc aaa gtc agg ccc aat ggg 351  
Arg Lys Arg Asp Trp Lys Lys Pro Glu Cys Lys Val Arg Pro Asn Gly  
80 85 90

agg aaa cgg aaa tgc ctg gcc tgc atc aaa ctg gcc tct gag gac aaa 399  
Arg Lys Arg Lys Cys Leu Ala Cys Ile Lys Leu Gly Ser Glu Asp Lys  
95 100 105

gtt ctg ggc cgg ttg gtc cac tgc ccc ata gag acc caa gtt ctg cgg 447  
Val Leu Gly Arg Leu Val His Cys Pro Ile Glu Thr Gln Val Leu Arg  
110 115 120 125

gag gct gag gag cac cag gag acc cag tgc ctc agg gtg cag cgg gct 495  
Glu Ala Glu Glu His Gln Glu Thr Gln Cys Leu Arg Val Gln Arg Ala  
130 135 140

ggg gag gac ccc cac agc ttc tac ttc cct gga cag ttc gcc ttc tcc 543  
Gly Glu Asp Pro His Ser Phe Tyr Phe Pro Gly Gln Phe Ala Phe Ser  
145 150 155

aag gcc ctg ccc cgc agc taa gccagcactg agctgcgtgg tgcctccagg 594  
Lys Ala Leu Pro Arg Ser  
160

accgctgccg gtggaacca gtggaagacc ccagccccca gggagaggac cccgttctat 654

ccccagccat gataataaag ctgctctccc agctgcctct c 695

<210> 13  
<211> 1451  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (105)..(1436)

<400> 13  
actgcctgga aacgggctgg gcctgcctcg gacgccgccg gtgtcgcgga ttctctttcc 60

gcccgtcca tggcggtgga tgcctgactg gaagcccagag tggg atg cgg ctg acg 116

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Met Arg Leu Thr  
1

cg	g	aag	cg	ctc	tgc	tcg	ttt	ctt	atc	gcc	ctg	tac	tgc	cta	ttc	tcc	164
Arg	Lys	Arg	Leu	Cys	Ser	Phe	Leu	Ile	Ala	Leu	Tyr	Cys	Leu	Phe	Ser		
5					10					15					20		
ctc	tac	gct	gcc	tac	cac	gtc	ttc	ttc	ggg	cgc	cgc	cgc	cag	gcg	ccg	212	
Leu	Tyr	Ala	Ala	Tyr	His	Val	Phe	Phe	Gly	Arg	Arg	Arg	Gln	Ala	Pro		
				25					30					35			
gcc	ggg	tcc	ccg	cg	ggc	ctc	agg	aag	ggg	gcg	gcc	ccc	gcg	cg	gag	260	
Ala	Gly	Ser	Pro	Arg	Gly	Leu	Arg	Lys	Gly	Ala	Ala	Pro	Ala	Arg	Glu		
			40					45					50				
aga	cgc	ggc	cga	gaa	cag	tcc	act	ttg	gaa	agt	gaa	gaa	tgg	aat	cct	308	
Arg	Arg	Gly	Arg	Glu	Gln	Ser	Thr	Leu	Glu	Ser	Glu	Glu	Trp	Asn	Pro		
		55					60					65					
tgg	gaa	gga	gat	gaa	aaa	aat	gag	caa	caa	cac	aga	ttt	aaa	act	agc	356	
Trp	Glu	Gly	Asp	Glu	Lys	Asn	Glu	Gln	Gln	His	Arg	Phe	Lys	Thr	Ser		
	70					75					80						
ctt	caa	ata	tta	gat	aaa	tcc	acg	aaa	gga	aaa	aca	gat	ctc	agt	gta	404	
Leu	Gln	Ile	Leu	Asp	Lys	Ser	Thr	Lys	Gly	Lys	Thr	Asp	Leu	Ser	Val		
85					90					95					100		
caa	atc	tgg	ggc	aaa	gct	gcc	att	ggc	ttg	tat	ctc	tgg	gag	cat	att	452	
Gln	Ile	Trp	Gly	Lys	Ala	Ala	Ile	Gly	Leu	Tyr	Leu	Trp	Glu	His	Ile		
				105					110					115			
ttt	gaa	ggc	tta	ctt	gat	ccc	agc	gat	gtg	act	gct	caa	tgg	aga	gaa	500	
Phe	Glu	Gly	Leu	Leu	Asp	Pro	Ser	Asp	Val	Thr	Ala	Gln	Trp	Arg	Glu		
			120					125					130				
gga	aag	tca	atc	gta	gga	aga	aca	cag	tac	agc	ttc	atc	act	ggt	cca	548	
Gly	Lys	Ser	Ile	Val	Gly	Arg	Thr	Gln	Tyr	Ser	Phe	Ile	Thr	Gly	Pro		
		135					140					145					
gct	gta	ata	cca	ggg	tac	ttc	tcc	gtt	gat	gtg	aat	aat	gtg	gta	ctc	596	
Ala	Val	Ile	Pro	Gly	Tyr	Phe	Ser	Val	Asp	Val	Asn	Asn	Val	Val	Leu		
	150					155					160						
att	tta	aat	gga	aga	gaa	aaa	gca	aag	atc	ttt	tat	gcc	acc	cag	tgg	644	
Ile	Leu	Asn	Gly	Arg	Glu	Lys	Ala	Lys	Ile	Phe	Tyr	Ala	Thr	Gln	Trp		
165					170					175					180		
tta	ctt	tat	gca	caa	aat	tta	gtg	caa	att	caa	aaa	ctc	cag	cat	ctt	692	
Leu	Leu	Tyr	Ala	Gln	Asn	Leu	Val	Gln	Ile	Gln	Lys	Leu	Gln	His	Leu		
				185					190					195			
gct	gtt	gtt	ttg	ctc	gga	aat	gaa	cat	tgt	gat	aat	gag	tgg	ata	aac	740	
Ala	Val	Val	Leu	Leu	Gly	Asn	Glu	His	Cys	Asp	Asn	Glu	Trp	Ile	Asn		
			200					205					210				
cca	ttc	ctc	aaa	aga	aat	gga	ggc	ttc	gtg	gag	ctg	ctt	ttc	ata	ata	788	
Pro	Phe	Leu	Lys	Arg	Asn	Gly	Gly	Phe	Val	Glu	Leu	Leu	Phe	Ile	Ile		
		215					220					225					
tat	gac	agc	ccc	tgg	att	aat	gac	gtg	gat	gtt	ttt	cag	tgg	cct	tta	836	
Tyr	Asp	Ser	Pro	Trp	Ile	Asn	Asp	Val	Asp	Val	Phe	Gln	Trp	Pro	Leu		
	230					235					240						

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gga gta gca aca tac agg aat ttt cct gtg gtg gag gca agt tgg tca Gly Val Ala Thr Tyr Arg Asn Phe Pro Val Val Glu Ala Ser Trp Ser 245 250 255 260	884
atg ctg cat gat gag agg cca tat tta tgt aat ttc tta gga acg att Met Leu His Asp Glu Arg Pro Tyr Leu Cys Asn Phe Leu Gly Thr Ile 265 270 275	932
tat gaa aat tca tcc aga cag gca cta atg aac att ttg aaa aaa gat Tyr Glu Asn Ser Ser Arg Gln Ala Leu Met Asn Ile Leu Lys Lys Asp 280 285 290	980
ggg aac gat aag ctt tgt tgg gtt tca gca aga gaa cac tgg cag cct Gly Asn Asp Lys Leu Cys Trp Val Ser Ala Arg Glu His Trp Gln Pro 295 300 305	1028
cag gaa aca aat gaa agt ctt aag aat tac caa gat gcc ttg ctt cag Gln Glu Thr Asn Glu Ser Leu Lys Asn Tyr Gln Asp Ala Leu Leu Gln 310 315 320	1076
agt gat ctc aca ttg tgc ccg gtc gga gta aac aca gaa tgc tat cga Ser Asp Leu Thr Leu Cys Pro Val Gly Val Asn Thr Glu Cys Tyr Arg 325 330 335 340	1124
atc tat gag gct tgc tcc tat ggc tcc att cct gtg gtg gaa gac gtg Ile Tyr Glu Ala Cys Ser Tyr Gly Ser Ile Pro Val Val Glu Asp Val 345 350 355	1172
atg aca gct ggc aac tgt ggg aat aca tct gtg cac cac ggt gct cct Met Thr Ala Gly Asn Cys Gly Asn Thr Ser Val His His Gly Ala Pro 360 365 370	1220
ctg cag tta ctc aag tcc atg ggt gct ccc ttt atc ttt atc aag aac Leu Gln Leu Leu Lys Ser Met Gly Ala Pro Phe Ile Phe Ile Lys Asn 375 380 385	1268
tgg aag gaa ctc cct gct gtt tta gaa aaa gag aaa act ata att tta Trp Lys Glu Leu Pro Ala Val Leu Glu Lys Glu Lys Thr Ile Ile Leu 390 395 400	1316
caa gaa aaa att gaa aga aga aaa atg tta ctt cag tgg tat cag cac Gln Glu Lys Ile Glu Arg Arg Lys Met Leu Leu Gln Trp Tyr Gln His 405 410 415 420	1364
ttc aag aca gag ctt aaa atg aaa ttt act aat att tta gaa agc tca Phe Lys Thr Glu Leu Lys Met Lys Phe Thr Asn Ile Leu Glu Ser Ser 425 430 435	1412
ttt tta atg aat aat aaa agt taa ttatcttttt gagct Phe Leu Met Asn Asn Lys Ser 440	1451

<210> 14  
<211> 72  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 14

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Met Ser Asp Ser Lys Glu Pro Arg Val Gln Gln Leu Gly Leu Leu Gly  
1 5 10 15

Cys Leu Gly His Gly Ala Leu Val Leu Gln Leu Leu Ser Phe Met Leu  
20 25 30

Leu Ala Gly Val Leu Val Ala Ile Leu Val Gln Val Ser Lys Val Pro  
35 40 45

Ser Ser Leu Ser Gln Glu Gln Ser Glu Gln Asp Ala Ile Tyr Gln Asn  
50 55 60

Leu Thr Gln Leu Lys Ala Ala Val  
65 70

<210> 15  
<211> 128  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct  
<400> 15

Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala  
1 5 10 15

Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro  
20 25 30

Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala  
35 40 45

Trp Pro Thr Pro Pro Thr Arg Pro Ala Pro Ala Pro Cys His Ala Asn  
50 55 60

Thr Ser Met Val Thr His Pro Asp Phe Ala Thr Gln Pro Gln His Val  
65 70 75 80

Gln Asn Phe Leu Leu Tyr Arg His Cys Arg His Phe Pro Leu Leu Gln  
85 90 95

Asp Val Pro Pro Ser Lys Cys Ala Gln Pro Val Phe Leu Leu Leu Val  
100 105 110

Ile Lys Ser Ser Pro Ser Asn Tyr Val Arg Arg Glu Leu Leu Arg Arg  
115 120 125

<210> 16

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<211> 50  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 16

Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly Ala Leu Leu Gly  
 1 5 10 15

Thr Ala Trp Ala Arg Arg Ser Gln Asp Leu His Cys Gly Ala Cys Arg  
 20 25 30

Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln Val Asp Pro Lys  
 35 40 45

Lys Thr  
 50

<210> 17  
 <211> 135  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Synthetic Construct

<400> 17

Met Arg Arg Leu Leu Ile Pro Leu Ala Leu Trp Leu Gly Ala Val Gly  
 1 5 10 15

Val Gly Val Ala Glu Leu Thr Glu Ala Gln Arg Arg Gly Leu Gln Val  
 20 25 30

Ala Leu Glu Glu Phe His Lys His Pro Pro Val Gln Trp Ala Phe Gln  
 35 40 45

Glu Thr Ser Val Glu Ser Ala Val Asp Thr Pro Phe Pro Ala Gly Ile  
 50 55 60

Phe Val Arg Leu Glu Phe Lys Leu Gln Gln Thr Ser Cys Arg Lys Arg  
 65 70 75 80

Asp Trp Lys Lys Pro Glu Cys Lys Val Arg Pro Asn Gly Arg Lys Arg  
 85 90 95

Lys Cys Leu Ala Cys Ile Lys Leu Gly Ser Glu Asp Lys Val Leu Gly  
 100 105 110

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Arg Leu Val His Cys Pro Ile Glu Thr Gln Val Leu Arg Glu Ala Glu  
115 120 125

Glu His Gln Glu Thr Gln Cys  
130 135

<210> 18  
<211> 148  
<212> PRT  
<213> Artificial

<220>  
<223> Synthetic Construct

<400> 18

Met Arg Leu Thr Arg Lys Arg Leu Cys Ser Phe Leu Ile Ala Leu Tyr  
1 5 10 15

Cys Leu Phe Ser Leu Tyr Ala Ala Tyr His Val Phe Phe Gly Arg Arg  
20 25 30

Arg Gln Ala Pro Ala Gly Ser Pro Arg Gly Leu Arg Lys Gly Ala Ala  
35 40 45

Pro Ala Arg Glu Arg Arg Gly Arg Glu Gln Ser Thr Leu Glu Ser Glu  
50 55 60

Glu Trp Asn Pro Trp Glu Gly Asp Glu Lys Asn Glu Gln Gln His Arg  
65 70 75 80

Phe Lys Thr Ser Leu Gln Ile Leu Asp Lys Ser Thr Lys Gly Lys Thr  
85 90 95

Asp Leu Ser Val Gln Ile Trp Gly Lys Ala Ala Ile Gly Leu Tyr Leu  
100 105 110

Trp Glu His Ile Phe Glu Gly Leu Leu Asp Pro Ser Asp Val Thr Ala  
115 120 125

Gln Trp Arg Glu Gly Lys Ser Ile Val Gly Arg Thr Gln Tyr Ser Phe  
130 135 140

Ile Thr Gly Pro  
145